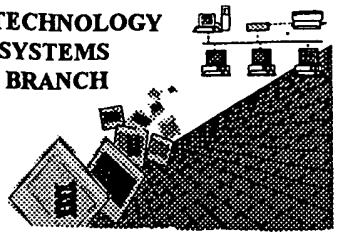
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

1652

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/697,186
Source: 1600
Date Processed by STIC: 2/22/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/697,186

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2____	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 ✓	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4____	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5____	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7____	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8____	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10____	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11____	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12____	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13____	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/697,186

DATE: 02/22/2002
TIME: 14:56:40

Input Set: I697186.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

RECEIVED
MAR 1 2 2002
TECH CENTER 1600/2900

pp 1-5

1 <110> RIKEN
2 <120> A MUTANT KANAMYCIN NUCLEOTIDYLTRANSFERASE AND A METHOD OF SCREENING
3 THERMOPHILIC BACTERIA USING THE SAME
4 <130> PH-1082
5 <140> US/09/697,186
6 <141> 2000-10-27
7 <150> JP 11-309616
8 <151> 29-OCT-1999
9 <160> 11
10 <170> PatentIn Ver. 2.0

ERRORED SEQUENCES FOLLOW

11 <210> 1
12 <211> 253
13 <212> PRT
14 <213> Artificial Sequence
15 <220>
16 <223> mutantenzyme obtained by introduction of point mutation into wild type KNT
17 gene of Staphylococcus aureus and its expression
18 <400> 1

```
19      Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
E--> 20   1  5        10          15
21      His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
22                  20                  25                  30
23      Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
24              35                  40                  45
25      Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu Phe
26          50                  55                  60
27      Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe Tyr
28      65                  70                  75                  80
29      Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp Trp
30                      85                  90                  95
31      Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp Ser
32                  100                 105                 110
33      Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
34              115                 120                 125
35      Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
36          130                 135                 140
37      Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
38      145                 150                 155                 160
39      Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
```

misaligned amino acid numbers (see item 3 on Error Summary Sheet)

```
40                  165                 170                 175
41  Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
42                  180                 185                 190
43  Thr Glu Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His Leu
44          195                 200                 205
45  Cys Gln Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu Leu
46      210                 215                 220
47  Glu Ser Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu Arg
48  225                 230                 235                 240
49  His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
50                  245                 250
```

---

delete these non-ASCII characters globally
They cause errors.

```
51  <210> 3
52  <211> 253
53  <212> PRT
54  <213> Artificial@Sequence
55  <220>
56  <223> mutant@enzyme@obtained@by@introduction@of@point mutation into wild
57        type KNT@gene of Staphylococcus aureus and its@expression
58  <400> 3
59        Met Lys Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile Val
60          1               5                  10                  15
61        His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val Lys
62                      20                  25                  30
63        Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro Tyr
64                  35                  40                  45
65        Ser Asp Ile Glu Met Met Cys Val Leu Ser Thr Glu Gly Val Glu Phe
E-->  66       50                  55  @@@@@ @@@60   misaligned NOS.
67        Ser Tyr Glu Trp Thr Thr Gly Glu Trp Lys Ala Glu Val Asn Phe Tyr
68         65                  70                  75                  80
69        Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Arg Val Glu Pro Asp Trp
70                      85                  90                  95
71        Pro Leu Thr His Gly Arg Phe Phe Ser Ile Leu Pro Ile Tyr Asp Pro
72                  100                 105                 110
73        Gly Gly Tyr Phe Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu Ala
74                  115                 120                 125
75        Gln Lys Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu Phe
76              130                 135                 140
77        Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr Thr
78        145                 150                 155                 160
79        Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met Leu
80                      165                 170                 175
81        Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val Leu
82                  180                 185                 190
83        Thr Glu Ala Val Lys Gln Pro Asp Leu Pro Pro Gly Tyr Val Gln Leu
84                  195                 200                 205
85        Cys Gln Leu Val Met Ser Gly Gln Leu Ser Asp Pro Glu Lys Leu Leu
86              210                 215                 220
87        Glu Ser Leu Glu Asn Phe Trp Asn Gly Val Gln Glu Trp Ala Glu Arg
88        225                 230                 235                 240
```

```
       89          His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro Phe
       90                          245                 250
```

```
       91    <210> 10
E-->   92    <211> 759
       93    <212> DNA
       94    <213> Staphylococcus aureus
       95    <220>
       96    <221> CDS
       97    <222> (1)..(759)
       98    <400> 10
E-->   99          gtg aat gga cca ata ata atg act aga gaa gaa aga atg aag att gtt      48 Met
W-->  100
      101          Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile
W-->  102            1               5                  10                  15
E-->  103          cat gaa att aag gaa cga ata ttg gat aaa tat ggg gat gat gtt aag      96 His
W-->  104
      105          Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val
W-->  106                      20                  25                  30
E-->  107          gct att ggt gtt tat ggc tct ctt ggt cgt cag act gat ggg ccc tat     144 Ala
W-->  108
      109          Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro
      110                   35                  40                  45
E-->  111          tcg gat att gag atg atg tgt gtc atg tca aca gag gaa gca gag ttc     192 Ser
W-->  112
      113          Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu
      114               50                  55                  60
E-->  115          agc cat gaa tgg aca acc ggt gag tgg aag gtg gaa gtg aat ttt gat     240 Ser
W-->  116
      117          Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe
W-->  118           65                  70                  75                  80
E-->  119          agc gaa gag att cta cta gat tat gca tct cag gtg gaa tca gat tgg     288 Ser
W-->  120
      121          Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp
W-->  122                      85                  90                  95
E-->  123          ccg ctt aca cat ggt caa ttt ttc tct att ttg ccg att tat gat tca     336 Pro
W-->  124
      125          Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp
      126                     100                 105                 110
E-->  127          ggt gga tac tta gag aaa gtg tat caa act gct aaa tcg gta gaa gcc     384 Gly
W-->  128
      129          Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu
      130                  115                 120                 125
E-->  131          caa acg ttc cac gat gcg att tgt gcc ctt atc gta gaa gag ctg ttt     432 Gln
W-->  132
      133          Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu
      134              130                 135                 140
E-->  135          gaa tat gca ggc aaa tgg cgt aat att cgt gtg caa gga ccg aca aca     480 Glu
W-->  136
      137          Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr
```

delete

see p. 4

insert hard return

```
W--> 138          145                 150                 155                 160
E--> 139  ttt cta cca tcc ttg act gta cag gta gca atg gca ggt gcc atg ttg     528 Phe
W--> 140
     141  Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met
W--> 142                165                 170                 175
E--> 143  att ggt ctg cat cat cgc atc tgt tat acg acg agc gct tcg gtc tta     576 Ile
W--> 144
     145  Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val
     146                180                 185                 190
E--> 147  act gaa gca gtt aag caa tca gat ctt cct tca ggt tat gac cat ctg     624 Thr
W--> 148
     149  Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His
     150          195                 200                 205
E--> 151  tgc cag ttc gta atg tct ggt caa ctt tcc gac tct gag aaa ctt ctg     672 Cys
W--> 152
     153  Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu
     154      210                 215                 220
E--> 155  gaa tcg cta gag aat ttc tgg aat ggg att cag gag tgg aca gaa cga     720 Glu
W--> 156
     157  Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu
W--> 158  225                 230                 235                 240
E--> 159  cac gga tat ata gtg gat gtg tca aaa cgc ata cca ttt               759 His
W--> 160
     161  Tyr Ile Val Asp Val Ser Lys Arg Ile Pro
W--> 162                245                 250
```

```
     163  <210> 11
E--> 164  <211> 253
     165  <212> PRT
     166  <213> Staphylococcus aureus
     167  <400> 11
     168        Met Asn Gly Pro Ile Ile Met Thr Arg Glu Glu Arg Met Lys Ile
     169          1               5                  10                  15
     170        His Glu Ile Lys Glu Arg Ile Leu Asp Lys Tyr Gly Asp Asp Val
     171                      20                  25                  30
     172        Ala Ile Gly Val Tyr Gly Ser Leu Gly Arg Gln Thr Asp Gly Pro
     173                  35                  40                  45
     174        Ser Asp Ile Glu Met Met Cys Val Met Ser Thr Glu Glu Ala Glu
     175              50                  55                  60
     176        Ser His Glu Trp Thr Thr Gly Glu Trp Lys Val Glu Val Asn Phe
     177            65                  70                  75                  80
     178        Ser Glu Glu Ile Leu Leu Asp Tyr Ala Ser Gln Val Glu Ser Asp
     179                          85                  90                  95
     180        Pro Leu Thr His Gly Gln Phe Phe Ser Ile Leu Pro Ile Tyr Asp
     181                      100                 105                 110
     182        Gly Gly Tyr Leu Glu Lys Val Tyr Gln Thr Ala Lys Ser Val Glu
     183                  115                 120                 125
     184        Gln Thr Phe His Asp Ala Ile Cys Ala Leu Ile Val Glu Glu Leu
     185              130                 135                 140
     186        Glu Tyr Ala Gly Lys Trp Arg Asn Ile Arg Val Gln Gly Pro Thr
```

? Please ensure 253 amino acids are shown in this sequence. delete

see p 5

misaligned nos.

```
                145                 150                 155                 160
Phe Leu Pro Ser Leu Thr Val Gln Val Ala Met Ala Gly Ala Met
                165                 170                 175
Ile Gly Leu His His Arg Ile Cys Tyr Thr Thr Ser Ala Ser Val
            180                 185                 190
Thr Glu Ala Val Lys Gln Ser Asp Leu Pro Ser Gly Tyr Asp His
        195                 200                 205
Cys Gln Phe Val Met Ser Gly Gln Leu Ser Asp Ser Glu Lys Leu
    210                 215                 220
Glu Ser Leu Glu Asn Phe Trp Asn Gly Ile Gln Glu Trp Thr Glu
225                 230                 235                 240
His Gly Tyr Ile Val Asp Val Ser Lys Arg Ile Pro
                245                 250
```

E--> @@@

E--> 1/14

misaligned nos.

delete

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/697,186**

DATE: 02/22/2002
TIME: 14:56:40

Input Set: **I697186.RAW**

Line	?	Error/Warning	Original Text
20	E	Invalid/Missing Amino Acid Numbering	1 5 10 15
66	E	Invalid/Missing Amino Acid Numbering	50 55 @@@@@ @@@60
92	E	Input 759, Calc# Bases 0 differ	<211> 759
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
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99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
99	E	Wrong Amino Acid Designator	gtg aat gga cca ata ata atg act aga gaa g
100	W	Invalid/Missing Amino Acid Numbering	
102	W	Invalid/Missing Amino Acid Numbering	1 5 10
103	E	Wrong Amino Acid Designator	cat gaa att aag gaa cga ata ttg gat aaa t
103	E	Wrong Amino Acid Designator	cat gaa att aag gaa cga ata ttg gat aaa t
103	E	Wrong Amino Acid Designator	cat gaa att aag gaa cga ata ttg gat aaa t
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103	E	Wrong Amino Acid Designator	cat gaa att aag gaa cga ata ttg gat aaa t
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107	E	Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
107	E	Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
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107	E	Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
107	E	Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
107	E	Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
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107 E Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
107 E Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c
107 E Wrong Amino Acid Designator	gct att ggt gtt tat ggc tct ctt ggt cgt c

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/697,186**

DATE: 02/22/2002
TIME: 14:56:40

Input Set: **I697186.RAW**

Line	?	Error/Warning	Original Text
108	W	Invalid/Missing Amino Acid Numbering	
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111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
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111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
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111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
111	E	Wrong Amino Acid Designator	tcg gat att gag atg atg tgt gtc atg tca a
112	W	Invalid/Missing Amino Acid Numbering	
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
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115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
115	E	Wrong Amino Acid Designator	agc cat gaa tgg aca acc ggt gag tgg aag g
116	W	Invalid/Missing Amino Acid Numbering	
118	W	Invalid/Missing Amino Acid Numbering	65 70
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c
119	E	Wrong Amino Acid Designator	agc gaa gag att cta cta gat tat gca tct c

Input Set: **I697186.RAW**

Line	?	Error/Warning	Original Text
120	W	Invalid/Missing Amino Acid Numbering	
122	W	Invalid/Missing Amino Acid Numbering	85 90
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
123	E	Wrong Amino Acid Designator	ccg ctt aca cat ggt caa ttt ttc tct att t
124	W	Invalid/Missing Amino Acid Numbering	
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
127	E	Wrong Amino Acid Designator	ggt gga tac tta gag aaa gtg tat caa act g
128	W	Invalid/Missing Amino Acid Numbering	
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a
131	E	Wrong Amino Acid Designator	caa acg ttc cac gat gcg att tgt gcc ctt a

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/697,186**

DATE: 02/22/2002
TIME: 14:56:40

Input Set: **I697186.RAW**

Line	?	Error/Warning	Original Text
132	W	Invalid/Missing Amino Acid Numbering	
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
135	E	Wrong Amino Acid Designator	gaa tat gca ggc aaa tgg cgt aat att cgt g
136	W	Invalid/Missing Amino Acid Numbering	
138	W	Invalid/Missing Amino Acid Numbering	145 150 1
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
139	E	Wrong Amino Acid Designator	ttt cta cca tcc ttg act gta cag gta gca a
140	W	Invalid/Missing Amino Acid Numbering	
142	W	Invalid/Missing Amino Acid Numbering	165 170
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a
143	E	Wrong Amino Acid Designator	att ggt ctg cat cat cgc atc tgt tat acg a

143 E Wrong Amino Acid Designator

att ggt ctg cat cat cgc atc tgt tat acg a

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/697,186**

DATE: 02/22/2002
TIME: 14:56:40

Input Set: **I697186.RAW**

Line	?	Error/Warning	Original Text
144	W	Invalid/Missing Amino Acid Numbering	
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
147	E	Wrong Amino Acid Designator	act gaa gca gtt aag caa tca gat ctt cct t
148	W	Invalid/Missing Amino Acid Numbering	
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
151	E	Wrong Amino Acid Designator	tgc cag ttc gta atg tct ggt caa ctt tcc g
152	W	Invalid/Missing Amino Acid Numbering	
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c
155	E	Wrong Amino Acid Designator	gaa tcg cta gag aat ttc tgg aat ggg att c

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/697,186**

DATE: 02/22/2002
TIME: 14:56:40

Input Set: **I697186.RAW**

Line	?	Error/Warning	Original Text
156	W	Invalid/Missing Amino Acid Numbering	
158	W	Invalid/Missing Amino Acid Numbering	225 230 2
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
159	E	Wrong Amino Acid Designator	cac gga tat ata gtg gat gtg tca aaa cgc a
160	W	Invalid/Missing Amino Acid Numbering	
162	W	Invalid/Missing Amino Acid Numbering	245 250
164	E	Input 253, Calc Seq.Length 254 differ	<211> 253
200	E	Wrong Amino Acid Designator	@@@
201	E	Invalid/Missing Amino Acid Numbering	1/14